

> file biosis medline caplus wpids uspatfull

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SINCE FILE

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ENTRY

SESSION

FULL ESTIMATED COST

2.20

2.20

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FILE 'CAPLUS' ENTERED AT 08:19:15 ON 04 JAN 2009

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*** YOU HAVE NEW MAIL ***

=> s time (7a) polymerase (7a) bind?

L1 209 TIME (7A) POLYMERASE (7A) BIND?

=> s l1 and sequence (4a) determin?

L2 44 L1 AND SEQUENCE (4A) DETERMIN?

=> s l2 and time (4a) polymerase (4a) bind?

L3 9 L2 AND TIME (4A) POLYMERASE (4A) BIND?

=> dup rem l3

PROCESSING COMPLETED FOR L3

L4 9 DUP REM L3 (0 DUPLICATES REMOVED)

=> d l4 bib abs 1-9

L4 ANSWER 1 OF 9 USPATFULL on STN

AN 2008:86990 USPATFULL

TI MODIFIED SURFACES FOR THE DETECTION OF BIOMOLECULES AT THE SINGLE
MOLECULE LEVEL

IN Belosludtsev, Yuri, The Woodlands, TX, UNITED STATES

Battulga, Nasanshargal, Houston, TX, UNITED STATES

Reddy, Mistu, Pearland, TX, UNITED STATES

Kraltcheva, Anelia, Houston, TX, UNITED STATES

Hardin, Susan H., College Station, TX, UNITED STATES

Lincecum, Tommie L. JR., Houston, TX, UNITED STATES

Wang, Hongyi, Houston, TX, UNITED STATES

Deluge, Norha, Houston, TX, UNITED STATES

Nagaswamy, Uma, Houston, TX, UNITED STATES

Stevens, Benjamin C., Houston, TX, UNITED STATES

Kincaid, Kristi K., Houston, TX, UNITED STATES

PA VISIGEN BIOTECHNOLOGIES, INC., Houston, TX, UNITED STATES (U.S.
corporation)

PI US 20080076189 A1 20080327

AI US 2007-694605 A1 20070330 (11)

PRAI US 2006-787434P 20060330 (60)

DT Utility

FS APPLICATION

LREP ROBERT W STROZIER, P.L.L.C, PO BOX 429, BELLAIRE, TX, 77402-0429, US

CLMN Number of Claims: 30
ECL Exemplary Claim: 1
DRWN 6 Drawing Page(s)
LN.CNT 1692

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Support surfaces are disclosed that are designed to support molecules or molecular assemblies immobilized thereon so that the molecules or molecular assemblies can be observed in single molecule detections systems, where the support surfaces have reduced background and the fluorescent labels associated with the immobilized molecules or molecular assemblies have longer active lifetimes prior to permanent photo-bleaching or deactivation and have improve fluorescence properties and where the surfaces have more uniform fluorescent properties.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 2 OF 9 USPATFULL on STN

AN 2008:80110 USPATFULL

TI Method for Sequencing Nucleic Acid Molecules

IN Densham, Daniel, Exeter, UNITED KINGDOM

PI US 20080070236 A1 20080320

AI US 2004-565750 A1 20040726 (10)

WO 2004-GB3232 20040726

20070228 PCT 371 date

PRAI GB 2003-17343 20030724

DT Utility

FS APPLICATION

LREP SALIWANCHIK LLOYD & SALIWANCHIK, A PROFESSIONAL ASSOCIATION, PO BOX 142950, GAINESVILLE, FL, 32614-2950, US

CLMN Number of Claims: 20

ECL Exemplary Claim: 1

DRWN 2 Drawing Page(s)

LN.CNT 567

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The sequence of a target polynucleotide can be determined by: (i) contacting the target polynucleotide with a polymerase enzyme and one of the nucleotides A, T(U), G, and C under conditions suitable for the polymerase reaction to proceed; (ii) measuring the time taken for the polymerase to bind to and subsequently dissociate from the target polynucleotide, to thereby determine whether the polymerase has incorporated the nucleotide onto the target polynucleotide; (iii) optionally repeating steps (i) and (ii) with additional nucleotides, to thereby identify the sequence of the target polynucleotide.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 3 OF 9 WPIDS COPYRIGHT 2009 THOMSON REUTERS on STN

AN 2005-123165 [13] WPIDS

DNC C2005-040939 [13]

TI Identifying the sequence or a mutation in a target polynucleotide, useful for identifying single nucleotide polymorphism, by measuring the time taken for a polymerase enzyme to bind and dissociate from the polynucleotide

DC B04; D16

IN DENSHAM D; DENSHAM D H; DENSHAM D H M

PA (MEDI-N) MEDICAL BIOSYSTEMS LTD; (DENS-I) DENSHAM D

CYC 107

PIA WO 2005010210 A2 20050203 (200513)* EN 19[1]

EP 1649051 A2 20060426 (200628) EN

MX 2006000962 A1 20060401 (200654) ES

BR 2004012813 A 20060926 (200665) PT
 AU 2004259893 A1 20050203 (200667) EN
 KR 2006052863 A 20060519 (200675) KO
 JP 2006528485 W 20061221 (200703) JA 15
 CN 1852991 A 20061025 (200715) ZH
 EP 1649051 B1 20080305 (200819) EN
 US 20080070236 A1 20080320 (200822) EN
 DE 602004012273 E 20080417 (200829) DE
 ES 2303083 T3 20080801 (200855) ES

ADT WO 2005010210 A2 WO 2004-GB3232 20040726; AU 2004259893 A1 AU 2004-259893 20040726; BR 2004012813 A BR 2004-12813 20040726; CN 1852991 A CN 2004-80026931 20040726; DE 602004012273 E DE 2004-602004012273 20040726; EP 1649051 A2 EP 2004-743561 20040726; EP 1649051 B1 EP 2004-743561 20040726; DE 602004012273 E EP 2004-743561 20040726; EP 1649051 A2 WO 2004-GB3232 20040726; MX 2006000962 A1 WO 2004-GB3232 20040726; BR 2004012813 A WO 2004-GB3232 20040726; KR 2006052863 A WO 2004-GB3232 20040726; JP 2006528485 W WO 2004-GB3232 20040726; EP 1649051 B1 WO 2004-GB3232 20040726; US 20080070236 A1 WO 2004-GB3232 20040726; DE 602004012273 E WO 2004-GB3232 20040726; JP 2006528485 W JP 2006-520906 20040726; KR 2006052863 A KR 2006-701539 20060123; MX 2006000962 A1 MX 2006-962 20060124; US 20080070236 A1 US 2007-565750 20070228; ES 2303083 T3 EP 2004-743561 20040726

FDT DE 602004012273 E Based on EP 1649051 A; EP 1649051 A2 Based on WO 2005010210 A; MX 2006000962 A1 Based on WO 2005010210 A; BR 2004012813 A Based on WO 2005010210 A; AU 2004259893 A1 Based on WO 2005010210 A; KR 2006052863 A Based on WO 2005010210 A; JP 2006528485 W Based on WO 2005010210 A; EP 1649051 B1 Based on WO 2005010210 A; DE 602004012273 E Based on WO 2005010210 A; ES 2303083 T3 Based on EP 1649051 A

PRAI GB 2003-17343 20030724

AN 2005-123165 [13] WPIDS

AB WO 2005010210 A2 UPAB: 20060121

NOVELTY - Identifying the sequence of or a mutation in a target polynucleotide by contacting the target polynucleotide with a polymerase enzyme and one of the nucleotides A, T (U), G and C and measuring the time taken for the polymerase to bind to and subsequently dissociate from the target polynucleotide to thus determine or identify whether the polymerase has incorporated the nucleotide onto the target polynucleotide or whether a mutation exists.

DETAILED DESCRIPTION - Identifying the sequence of or a mutation in a target polynucleotide comprises:

(a) contacting the target polynucleotide with a polymerase enzyme and one of the nucleotides A, T (U), G and C under conditions for the polymerase reaction to proceed;

(b) measuring the time taken for the polymerase to bind to and subsequently dissociate from the target polynucleotide, to thus determine or identify whether the polymerase has incorporated the nucleotide onto the target polynucleotide, and with reference to the native sequence of the target, determine whether a mutation exists;

(c) optionally repeating steps (a) and (b) with additional nucleotides, to thus identify the sequence of the target polynucleotide.

USE - The method is useful for identifying the complete target polynucleotide sequence or the sequence of a part of the polynucleotide. It is particularly useful for determining the presence of mutations within the target e.g. determining whether a substitution, deletion or addition has occurred compared to a control or reference sequence, specifically for identifying a single nucleotide polymorphism in a genetic sample and thus determine the identity of the nucleotide(s) at the putative site of mutation.

L4 ANSWER 4 OF 9 USPATFULL on STN
AN 2004:203348 USPATFULL
TI Method for detection of multiple nucleic acid sequence variations
IN Quinn, John J., Concord, CA, UNITED STATES
Warner, Brian D., Martinez, CA, UNITED STATES
Weare, John, El Sobrante, CA, UNITED STATES
PI US 20040157238 A1 20040812
AI US 2003-666744 A1 20030915 (10)
PRAI US 2002-412477P 20020920 (60)
DT Utility
FS APPLICATION
LREP REED & EBERLE LLP, 800 MENLO AVENUE, SUITE 210, MENLO PARK, CA, 94025
CLMN Number of Claims: 37
ECL Exemplary Claim: 1
DRWN 4 Drawing Page(s)
LN.CNT 1319
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method for detecting the presence or absence of a genetic variation at a polymorphic site in a nucleic acid analyte in a sample is provided. The method comprises a series of steps used to form captured wild type complexes and captured variant complexes that are detected and counted. The method is carried out using first and second differential hybridization probes, first and second capture probes, and first and second solid substrates, each having a detectable signal. The invention also provides for kits for carrying out the assay.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 5 OF 9 USPATFULL on STN
AN 2003:237907 USPATFULL
TI Compositions and methods for the therapy and diagnosis of colon cancer
IN King, Gordon E., Shoreline, WA, UNITED STATES
Meagher, Madeleine Joy, Seattle, WA, UNITED STATES
Xu, Jiangchun, Bellevue, WA, UNITED STATES
Secrist, Heather, Seattle, WA, UNITED STATES
Jiang, Yuqiu, Kent, WA, UNITED STATES
PA Corixa Corporation, Seattle, WA, UNITED STATES, 98104 (U.S. corporation)
PI US 20030166064 A1 20030904
AI US 2002-99926 A1 20020314 (10)
RLI Continuation-in-part of Ser. No. US 2001-33528, filed on 26 Dec 2001, PENDING Continuation-in-part of Ser. No. US 2001-920300, filed on 31 Jul 2001, PENDING
PRAI US 2001-302051P 20010629 (60)
US 2001-279763P 20010328 (60)
US 2000-223283P 20000803 (60)
DT Utility
FS APPLICATION
LREP SEED INTELLECTUAL PROPERTY LAW GROUP PLLC, 701 FIFTH AVE, SUITE 6300, SEATTLE, WA, 98104-7092
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 8531
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Compositions and methods for the therapy and diagnosis of cancer, particularly colon cancer, are disclosed. Illustrative compositions comprise one or more colon tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention

and/or treatment of diseases, particularly colon cancer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 6 OF 9 USPATFULL on STN
AN 2003:106233 USPATFULL
TI Compositions and methods for the therapy and diagnosis of pancreatic cancer
IN Benson, Darin R., Seattle, WA, UNITED STATES
Kalos, Michael D., Seattle, WA, UNITED STATES
Lodes, Michael J., Seattle, WA, UNITED STATES
Persing, David H., Redmond, WA, UNITED STATES
Hepler, William T., Seattle, WA, UNITED STATES
Jiang, Yuqiu, Kent, WA, UNITED STATES
PA Corixa Corporation, Seattle, WA, UNITED STATES, 98104 (U.S. corporation)
PI US 20030073144 A1 20030417
AI US 2002-60036 A1 20020130 (10)
PRAI US 2001-333626P 20011127 (60)
US 2001-305484P 20010712 (60)
US 2001-265305P 20010130 (60)
US 2001-267568P 20010209 (60)
US 2001-313999P 20010820 (60)
US 2001-291631P 20010516 (60)
US 2001-287112P 20010428 (60)
US 2001-278651P 20010321 (60)
US 2001-265682P 20010131 (60)
DT Utility
FS APPLICATION
LREP SEED INTELLECTUAL PROPERTY LAW GROUP PLLC, 701 FIFTH AVE, SUITE 6300, SEATTLE, WA, 98104-7092
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 14253

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Compositions and methods for the therapy and diagnosis of cancer, particularly pancreatic cancer, are disclosed. Illustrative compositions comprise one or more pancreatic tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly pancreatic cancer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 7 OF 9 USPATFULL on STN
AN 2002:272801 USPATFULL
TI Compositions and methods for the therapy and diagnosis of colon cancer
IN Stolk, John A., Bothell, WA, UNITED STATES
Xu, Jiangchun, Bellevue, WA, UNITED STATES
Chenault, Ruth A., Seattle, WA, UNITED STATES
Meagher, Madeleine Joy, Seattle, WA, UNITED STATES
PA Corixa Corporation, Seattle, WA, UNITED STATES, 98104 (U.S. corporation)
PI US 20020150922 A1 20021017
AI US 2001-998598 A1 20011116 (9)
PRAI US 2001-304037P 20010710 (60)
US 2001-279670P 20010328 (60)
US 2001-267011P 20010206 (60)
US 2000-252222P 20001120 (60)
DT Utility

FS APPLICATION
LREP SEED INTELLECTUAL PROPERTY LAW GROUP PLLC, 701 FIFTH AVE, SUITE 6300,
SEATTLE, WA, 98104-7092
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 9233

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Compositions and methods for the therapy and diagnosis of cancer, particularly colon cancer, are disclosed. Illustrative compositions comprise one or more colon tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly colon cancer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 8 OF 9 USPATFULL on STN
AN 2002:243051 USPATFULL
TI Compositions and methods for the therapy and diagnosis of ovarian cancer
IN Algate, Paul A., Issaquah, WA, UNITED STATES
Jones, Robert, Seattle, WA, UNITED STATES
Harlocker, Susan L., Seattle, WA, UNITED STATES
PA Corixa Corporation, Seattle, WA, UNITED STATES, 98104 (U.S. corporation)
PI US 20020132237 A1 20020919
AI US 2001-867701 A1 20010529 (9)
PRAI US 2000-207484P 20000526 (60)
DT Utility
FS APPLICATION
LREP SEED INTELLECTUAL PROPERTY LAW GROUP PLLC, 701 FIFTH AVE, SUITE 6300,
SEATTLE, WA, 98104-7092
CLMN Number of Claims: 11
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 25718

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Compositions and methods for the therapy and diagnosis of cancer, particularly ovarian cancer, are disclosed. Illustrative compositions comprise one or more ovarian tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly ovarian cancer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 9 OF 9 USPATFULL on STN
AN 2002:242791 USPATFULL
TI Compositions and methods for the therapy and diagnosis of colon cancer
IN King, Gordon E., Shoreline, WA, UNITED STATES
Meagher, Madeleine Joy, Seattle, WA, UNITED STATES
Xu, Jiangchun, Bellevue, WA, UNITED STATES
Secrist, Heather, Seattle, WA, UNITED STATES
PA Corixa Corporation, Seattle, WA, UNITED STATES (U.S. corporation)
PI US 20020131971 A1 20020919
AI US 2001-33528 A1 20011226 (10)
RLI Continuation-in-part of Ser. No. US 2001-920300, filed on 31 Jul 2001,
PENDING

PRAI US 2001-302051P 20010629 (60)
US 2001-279763P 20010328 (60)
US 2000-223283P 20000803 (60)
DT Utility
FS APPLICATION
LREP SEED INTELLECTUAL PROPERTY LAW GROUP PLLC, 701 FIFTH AVE, SUITE 6300,
SEATTLE, WA, 98104-7092
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 8083

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Compositions and methods for the therapy and diagnosis of cancer, particularly colon cancer, are disclosed. Illustrative compositions comprise one or more colon tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly colon cancer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 14 4 kwic

L4 ANSWER 4 OF 9 USPATFULL on STN

SUMM [0001] This invention relates generally to a method for determining the sequence of a nucleic acid target at a polymorphic site. More specifically, the invention relates to a method of determining sequences. . . .

SUMM . . . examining these variations, scientists have been able to correlate specific traits, conditions, or diseases to particular variations in the genetic sequence. Consequently, determination of a genetic sequence at a particular location, commonly referred to as a polymorphic site, can enable the diagnosis of certain genetic diseases, and. . . .

SUMM [0003] Several techniques for determining the particular sequence at a polymorphic site have been reported in the literature. Specific methods include those based on oligonucleotide ligation and primer. . . .

SUMM . . . and the other complementary to the natural or "wild type" sequence. Based on the hybridization results, it is possible to determine which sequence, i.e., the variant or wild type, is contained in the target. A specific example of this technique is described in. . . .

SUMM . . . passed through a flow cytometer for detection of the label from the originally hybridized complementary labeled oligonucleotide (if present) and determination of the bead type. Sequence differentiation is based on whether the label from the originally hybridized complementary labeled probe is detected from the captured complex:. . . .

SUMM . . . each bead. Thus, while multiplexing is nonetheless possible with this approach, such competitive hybridization assays are not easily adaptable for sequence determination at other sites. Thus, there remains a need to provide assays that determine nucleic acid sequences easily and in a. . . .

DETD . . . via hydrogen bonds to complementary sequences. Finally, the temperature of the mixture is increased to about 72° C., during which time the polymerase binds and extends a complementary strand from each primer. Since the sequence

being amplified doubles after each sample, a theoretical amplification.

DETD . . . of captured variant complexes is indicative of the presence of the variation. Relative comparisons such as these are sufficient to determine the sequence at a known polymorphic site. Additional techniques can be used, however, to obtain even more information.

DETD . . . determined using standard techniques known in the art. For each of the differential hybridization probes, it is first necessary to determine the sequence for each polymorphic site, i.e., the wild type and variant sequences. The wild type and variant sequences can be determined. . . the relevant texts and databases providing wild type and variant sequences, such as the GenBank database (Bethesda, Md.). Once a sequence has been determined , the corresponding complementary sequence is included in the appropriate differential hybridization probe. That is, a region complementary to the polymorphic site corresponding to the. . .

=>